

**REMARKS**

In the Office Communication mailed on July 1, 2003, the Examiner requested a substitute sequence listing containing the amino acid sequences presented in Figure 1 and on pages 17 and 18 of the specification. The amino acid sequences presented in Figure 1 have been added to the sequence listing as SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16 and SEQ ID NO:17 in response to Examiner's request. SEQ ID NO:11 corresponds to  $\alpha$ q (WTq) in Figure 1. SEQ ID NO:12 corresponds to -6q in Figure 1. SEQ ID NO:13 corresponds to  $\alpha$ 11 in Figure 1. SEQ ID NO:14 corresponds to  $\alpha$ i1,3 in Figure 1. SEQ ID NO:15 corresponds to  $\alpha$ o1,2 in Figure 1. SEQ ID NO:16 corresponds to  $\alpha$ t1 in Figure 1. SEQ ID NO:17 corresponds to  $\alpha$ s in Figure 1.

In addition, SEQ ID NO:2, SEQ ID NO:4, and SEQ ID NO:8, have been amended and correspond to the sequences on pages 17 and 18 of the specification that the Examiner requested.

As described in the specification, the hybrid-G-protein  $\alpha$  subunits -6qi4 and -6qs5 lack the six highly conserved amino acids of the wild type  $\alpha$  subunit. Thus, rather than having the wild type amino acid sequence of MTLES at the amino terminus (as presented in Figure 1 and in SEQ ID NO:11), the amino terminus of both -6qi4 and -6qs5 begin with the sequence MACCL, which corresponds to the amino terminus of the wild type amino acid sequence starting at the seventh amino acid. (Paragraphs 058 and 059 on pages 16 and 17 of the specification describe the construction of -6qi4 and -6qs5.) In contrast, the hybrid-G-protein  $\alpha$  subunits -6qi4myr and -6qs5myr each

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contain a myristolation/palmitolation consensus sequence at their amino terminus, such that the first four amino acids at the amino terminus of -6qi4myr and -6qs5myr are MGCC, as opposed to MACC in -6qi4 and -6qs5. Paragraph 062 on pages 17 and 18 of the specification describes the construction of -6qi4myr and -6qs5myr and notes that their amino termini are MGCC as a result of the myristolation/palmitolation consensus sequence. The -6qi4myr and -6qi4 amino acid sequences contain the  $\alpha_i$  sequence at their carboxy termini, while -6qs5myr and -6qs5 amino acid sequences contain the  $\alpha_s$  sequence at their carboxy termini. The  $\alpha_s$  and  $\alpha_i$  sequences are well known in the art. (See e.g., Conklin et al., "Substitution of Three Amino Acids Switches Receptor Specificity of  $G_q\alpha$  to that of  $G_i\alpha$ ," *Nature* 363: 274-276 (1993) for a description of the analogous human proteins. This paper is disclosed on page 4 of the specification and is submitted in the attached Information Disclosure Statement).

SEQ ID NO:2 as originally filed on July 6, 2001 presented the wild type sequence rather than the -6qi4myr sequence. The amended SEQ ID NO:2 presents the -6qi4myr sequence. This error would have been obvious to one skilled in the art based on the specification and the prior art, since the amino terminus of SEQ ID NO:2 as originally filed was MTLES, rather than MGCC, and the carboxy terminus did not correspond to the five carboxy terminal amino acids of  $\alpha_i$ .

SEQ ID NO:4 as originally filed on July 6, 2001 presented the -6qi4myr sequence rather than the -6qs5myr sequence. The amended SEQ ID NO:4 presents the -6qs5myr sequence. It is known in the art that the final five amino acids of the  $\alpha_s$  sequence are QYELL. (See e.g., Conklin et al., "Substitution of Three Amino Acids

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Switches Receptor Specificity of  $G_q\alpha$  to that of  $G_i\alpha$ ," *Nature* 363: 274-276 (1993) for a description of the analogous human proteins). Again, it would have been obvious to one skilled in the art that SEQ ID NO:4 as originally filed was incorrect, since the final five amino acids were ECGLF, rather than QYELL.

SEQ ID NO:8 as originally filed on July 6, 2001 presented the -6qi4 sequence rather than the -6qs5 sequence. As stated above, the final five amino acids of the  $\alpha$ s sequence were known in the art as QYELL. Thus, it would have been obvious to one skilled in the art that SEQ ID NO:8 as originally filed was incorrect, since the final five amino acids were ECGLF, rather than QYELL.

In the specification, paragraph 031 has been amended to correct an inadvertent, typographical error.

The amended sequence listing is supported by the specification as a whole, and does not contain new matter. Case law further supports the proposition that the amended sequence listing is not new matter. For example, in *Reister v. Kendall*, the Court of Customs and Patent Appeals held that "a sufficient disclosure of patentable subject matter in a . . . specification will not be held to be insufficient for constructive reduction to practice by reason of a mistake in that specification which is obvious to any person skilled in the art." 34 C.C.P.A. 859, 863 (CCPA 1947). In a more recent case, the Board of Patent Appeals and Interferences discussed the correction of a sequencing error in a patent application. *Ex parte Maizel*, 27 U.S.P.Q.2d 1662 (Bd. Pat. App. & Int. 1992). The court noted that "the issue that must be broached in this and any other case is whether the description of the claimed compound in the original disclosure is

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adequate to identify and distinguish the claimed subject matter." *Id.* at 1667. Therefore, the amended sequence listing does not contain new matter, as the mistakes in the sequence listing would have been obvious to one skilled in the art and because the specification illustrates to those with skill in the art that Applicant was in possession of the invention as of the filing date.

Please grant any extensions of time required to enter this response and charge any required fees not found herewith to Deposit Account 06-0916.

Respectfully submitted,

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Attachments: Sequence listing in paper format  
Sequence listing in computer-readable format

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